1600

CRF Problem Report



The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

#13

Application Serial Number: 09/758,5256Filing Date: 1/10/2001Date Processed by STIC: 1/14/2002

STIC Contact: Mark Spencer, 703-308-4212

RECEIVED

NOV 1 2 2002

TECH CENTER 1600/2900

The CRF (was):		
	M	

(circle one) Damaged or Unreadable (for Unreadable, see attached)

Blank (no files on CRF) (see attached)

__ Empty file (filename present, but no bytes in file) (see attached)

___ Virus-infected. Virus name: ____ The STIC will not process the CRF.

___ Not saved in ASCII text

Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.

Did not contain a Sequence Listing. (see attached sample)

Other:

Nature of Problem:

PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS. SEE BELOW FOR ADDRESS:

http:/www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/758,52

1	Wrapped Nucleics	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
٠	_ vvrapped redictions	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it.		
		Please adjust your right margin to .3, as this will prevent "wrapping".		
2	_ Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line.		
		This may occur if your file was retrieved in a word processor after creating it.		
		Please adjust your right margin to .3, as this will prevent "wrapping".		
3	_ Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.		
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs		
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.		
5	_ Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.		
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.		
6	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.		
		As per the rules, each n or Xaa can only represent a single residue.		
		Please present the maximum number of each residue having variable length and		
		indicate in the (ix) feature section that some may be missing.		
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid		
		sequence(s) Normally, Patentin would automatically generate this section from the		
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section		
		to the subsequent amino acid sequence. This applies primarily to the mandatory <220>~223>		
		sections for Artificial or Unknown sequences.		
8	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:		
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:		
		(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")		
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:		
		This sequence is intentionally skipped		
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).		
9	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.		
	(NEW RULES)	<210> sequence id number		
		<400> sequence id number		
	/	000		
10	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing		
	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are present.		
		In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.		
11	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.		
	(NEW RULES)			
12	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.		
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"		
		Please explain source of genetic material in <220> to <223> section.		
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)		
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted		
		file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).		
		Instead, please use "File Manager" or any other means to copy file to floppy disk.		

OIPE

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Does Not Comply
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